

Db 61 FCYIILNLAADLFLFMSASTLSLETOPLVNTTDKHELMKLMFAVYVGLSLTAIS 120
121 TORCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDRCRVD 180
121 TORCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDRCRVD 180
181 VQALINGVLPVMTLSLTLFWVRRSSQOMRQPRFLRVVLAASVLPVLSLPLSTY 240
181 VQALINGVLPVMTLSLTLFWVRRSSQOMRQPRFLRVVLAASVLPVLSLPLSTY 240
241 MFLVYMTSLPEMQLCFSLSSSVSSANPVYILVSSRRSHLPPTSLSGLVQOAL 300
241 MFLVYMTSLPEMQLCFSLSSSVSSANPVYILVSSRRSHLPPTSLSGLVQOAL 300
301 REPELEGGETPTVTNEMGA 321
301 REPELEGGETPTVTNEMGA 321

RESULT 2

US-09-254-227A-13
Sequence 13, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254, 227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-227A-13

Query Match 32.8%; Score 544.5; DB 2; Length 322;
Best Local Similarity 41.9%; Pred. No. 2,6e-41;
Matches 134; Conservative 56; Mismatches 105; Indels 25; Gaps 10;

QY 1 MNQTLNNSGTVESALNYSRGSTVHTAYLVLSLAFCLCGMAGNSMTWILGPRMHRNP 60
1 MDPYVPLVGTGKLTPINGRETPCYNOTLSFTVLTCTISLVGTGNAVAVMLLGYMRNA 60
QY 61 FCYIILNLAADLFLFMSASTLSLETOP--LVNTTDKHELMKLMFAVYVGLSLTA 118
61 VSIYILNLAADFLF-----SFQIRSLRLINSHLRKILVSMFPFYTGLSMISA 115
QY 119 ISTORCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDR--CF 176
119 ISTORCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDR--CF 176
116 ISTERCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDR--CF 174
116 ISTERCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDR--CF 174
QY 177 RVDWQOALIMVLPVMTLSLTLFWVRRSSQOMRQPRFLRVVLAASVLPVLSLPLSTY 235
177 RVDWQOALIMVLPVMTLSLTLFWVRRSSQOMRQPRFLRVVLAASVLPVLSLPLSTY 235
175 TSDFLPVVLI-FLCVLVCVSSVLVLRILCS--RKNPLRLVYVTLILVAVLGLCL 230
175 TSDFLPVVLI-FLCVLVCVSSVLVLRILCS--RKNPLRLVYVTLILVAVLGLCL 230
QY 236 PLSIYFWLVYMTSLPE-----MOVLCFSLSLSSSVSSANPVYILVSSRRSHLPTR 290
236 PLSIYFWLVYMTSLPE-----MOVLCFSLSLSSSVSSANPVYILVSSRRSHLPTR 290
Db 231 PFGILGALYRMLNLEVLYCHVLYVCMGL-----SSLNSANPIIYFFGSGFR-QORNQ 285
231 PFGILGALYRMLNLEVLYCHVLYVCMGL-----SSLNSANPIIYFFGSGFR-QORNQ 285
QY 291 SLGTVLQOALREPELEGE 310
291 SLGTVLQOALREPELEGE 310
Db 286 NLKVLVQRALQDKPEVDKGE 305
286 NLKVLVQRALQDKPEVDKGE 305

RESULT 3

US-09-254-227A-11
Sequence 11, Application US/09254227A
Patent No. 6696257
GENERAL INFORMATION:
APPLICANT: Ahmad, Sultan
APPLICANT: Banville, Denis
APPLICANT: Fortin, Yves
APPLICANT: Lembo, Paola
APPLICANT: O'Donnell, Dajan
APPLICANT: Shi-Hsiang, Shen
TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
FILE REFERENCE: 81823/268117
CURRENT APPLICATION NUMBER: US/09/254, 227A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 322
TYPE: PRT
ORGANISM: Homo sapiens
US-09-254-227A-11

Query Match 32.5%; Score 539.5; DB 2; Length 322;
Best Local Similarity 42.4%; Pred. No. 7,5e-41;
Matches 137; Conservative 54; Mismatches 101; Indels 31; Gaps 12;

QY 1 MNQTLNNSGTVESALNYSRGSTVHTAYLVLSLAFCLCGMAGNSMTWILGPRMHRNP 57
1 MDPYVPLVGTGKLTPI--GRETEPCYNOTLSFTVLTCTISLVGTGNAVAVMLLGCRRK 57
QY 58 RNPFCYIILNLAADLFLFMSASTLSLETOP--LVNTTDKHELMKLMFAVYVGLSL 115
58 RNPFCYIILNLAADLFLFMSASTLSLETOP--LVNTTDKHELMKLMFAVYVGLSL 115
Db 58 RNPFCYIILNLAADLFLFMSASTLSLETOP--LVNTTDKHELMKLMFAVYVGLSL 112
58 RNPFCYIILNLAADLFLFMSASTLSLETOP--LVNTTDKHELMKLMFAVYVGLSL 112
QY 116 LNAISTORCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDR- 174
116 LNAISTORCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDR- 174
Db 113 LNAISTORCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDR- 171
113 LNAISTORCLSVLPFWKCHPRHLSAMVCGILMTLCLMNGLTSPFCKLKNEDR- 171
QY 175 -CRVVMQOALIMVLPVMTLSLTLFWVRRSSQOMRQPRFLRVVLAASVLPVLI 232
175 -CRVVMQOALIMVLPVMTLSLTLFWVRRSSQOMRQPRFLRVVLAASVLPVLI 232
Db 172 WCETSDFLPVVLI-FLCVLVCVSSVLVLRILCS--RKNPLRLVYVTLILVAVLGL 227
172 WCETSDFLPVVLI-FLCVLVCVSSVLVLRILCS--RKNPLRLVYVTLILVAVLGL 227
QY 233 CSLPLSYFWLVYMTSLPE-----MOVLCFSLSLSSSVSSANPVYILVSSRRSHLP 287
233 CSLPLSYFWLVYMTSLPE-----MOVLCFSLSLSSSVSSANPVYILVSSRRSHLP 287
Db 228 CGPPLGALYRMLNLEVLYCHVLYVCMGL-----SSLNSANPIIYFFGSGFR-QOR 282
228 CGPPLGALYRMLNLEVLYCHVLYVCMGL-----SSLNSANPIIYFFGSGFR-QOR 282
QY 288 PTRSLGTVLQOALREPELEGE 310
288 PTRSLGTVLQOALREPELEGE 310
Db 283 NRQNLKVLVQRALQDKPEVDKGE 305
283 NRQNLKVLVQRALQDKPEVDKGE 305

RESULT 4

US-10-314-048A-20
Sequence 20, Application US/10314048A
Patent No. 6902902
GENERAL INFORMATION:
APPLICANT: Unect, David J.
APPLICANT: Chen, Kuoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Dang, Huang T.
APPLICANT: Choi, Bryan
APPLICANT: Leonard, James
APPLICANT: Hakak, Yaron
APPLICANT: Liaw, Chen
APPLICANT: Lowitz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
FILE REFERENCE: 22,056,017
CURRENT APPLICATION NUMBER: US/10/314,048A

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 09:52:19 ; Search time 40 Seconds
(without alignments)
772.140 Million cell updates/sec

Title: US-10-509-484-4

Perfect score: 1661

Sequence: 1 MNQTLNSSGTVESALNYSRG.....EPELEGGETPTVGTNEMGA 321

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_80: *
2: p1r1: *
3: p1r2: *
4: p1r3: *
5: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465.5	28.0	343	2	A35639
2	461	27.8	324	1	TVRTAS
3	438.5	26.4	325	1	TVHUS
4	437	26.3	324	2	TVHUS
5	402.5	24.2	378	2	A39485
6	263.5	15.9	351	1	A46525
7	257.5	15.5	353	2	C42009
8	241.5	14.5	352	1	S27357
9	240.5	14.5	350	1	A37963
10	230	13.8	371	2	UC5498
11	228	13.7	352	2	A46520
12	218.5	13.2	371	2	UC5796
13	214.5	12.9	364	2	A49542
14	208	12.5	353	2	UC2492
15	206.5	12.4	351	2	B42009
16	202.5	12.2	391	2	A41795
17	202.5	12.2	391	2	C41795
18	202.5	12.2	391	2	A39297
19	201.5	12.1	482	2	S65766
20	196	11.8	369	2	D41795
21	195	11.7	346	2	S29248
22	193.5	11.6	369	2	UC5715
23	193	11.6	369	2	A45291
24	192	11.6	355	2	A55733
25	191.5	11.5	369	2	UC2083
26	190.5	11.4	369	2	UC5068
27	189.5	11.4	428	2	S30508
28	189	11.4	428	2	A39714
29	188.5	11.3	418	2	A46226

30	188	11.3	363	2	I57940	somatostatin recep
31	187.5	11.3	388	2	UN0605	somatostatin recep
32	187	11.3	350	2	A42009	N-formyl peptide r
33	186.5	11.2	359	2	A48921	interleukin-8 rece
34	186.5	11.2	369	2	B41795	somatostatin recep
35	185	11.1	362	2	A30341	G protein-coupled
36	183.5	11.0	346	2	UC5716	G protein-coupled
37	183	11.0	384	2	A47249	brain-specific som
38	182.5	11.0	428	2	A44021	somatostatin recep
39	179.5	10.8	355	2	JO1231	interleukin-8 rece
40	179	10.8	363	2	I57955	somatostatin recep
41	179	10.8	364	2	UN0763	somatostatin recep
42	178.5	10.7	350	2	A39445	interleukin-8 rece
43	176.5	10.6	356	2	S42096	interleukin-8 rece
44	176	10.6	360	2	A53611	interleukin-8 rece
45	176	10.6	473	2	UC5835	anaphylatoxin C3a

ALIGNMENTS

RESULT 1

A35639 G protein-coupled receptor RTA - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C/Accession: A35639

R/Rose, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Harcus, D.R.; Lynch, K

Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990

A/Title: RTA, a candidate G protein-coupled receptor: cloning, sequencing, and tissue di

A/Reference number: A35639; PMID:90222168; PMID:2109324

A/Accession: A35639

A/Molecule type: mRNA

A/Residues: 1-343 <ROS>

A/Cross-references: UNIPROT:P23749; UNIPARC:UP10000046P10; GB:M35297; NID:G206809; PIDN:

C/Keywords: G protein-coupled receptor; glycoprotein; membrane protein

F/4/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.0%; Score 465.5; DB 2; Length 343;

Best Local Similarity 35.7%; Pred. No. 7.4e-33;

Matches 121; Conservative 59; Mismatches 122; Indels 37; Gaps 11;

QY	2	NTLNSSGTVESALNYSRGSTVHTAVLVLSLA-----MFTCLCGAGNSMVI	49
DB	13	NQMKCPGSEALYLSRG-----FLITEQIATLPPAVNTYIFLLCLCGVNGVL	66
QY	50	WLGFPMHNPFCIYILNIAADLLFLPSMA--STLSLETOPLVNTDKVHELMKRLMYF	107
DB	67	WFGFSEIKRTPSIVYFLHLSADGIVLFSKAVIALINMGTFLGSPFDYRHRVSRIVGLC	125
QY	108	AYIVGSLTLTAISTQCSVLFPIMFKRPHRLSAMVGLMTCLMNGLTSSFCSEF	167
DB	126	TFPAGVSLPLPAISIERKCVSIFPMYWRPRRLSAGVALLMLLSFLVTSIHNFCC	184
QY	168	L--KFNEDRCFRVDMQOALINGVLPVMTLSLFLFVVRSSOQMRPRLFFVVL	225
DB	185	LGRBASGTCLAMNDISLGLLFLFPLMVLPCALILVERRAR--KORSKALNHVLA	243
QY	226	SVLVFLICLPISIVFWVYLSLP---PEMQVLCFSRLSSVSSANPIYFLVGSR	282
DB	244	IYVFLVSSIVYIGIDWFLFWFQIPAPPEY-----VTDLCICINSSAKPIVYFLAGND	297
QY	283	RSRRLPRLSLGTYLQALRE--EPELEGGETPTVGTNEM	319
DB	298	KSQRL--WEPLRVFORLRDGAEPDPASTENTVTEM	335

RESULT 2

transforming protein mas - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004

C:Accession: A31816
 R:Young, D.; O'Neill, K.; Jessell, T.; Wigler, M.
 Proc. Natl. Acad. Sci. U.S.A. 85, 5333-5342, 1988
 A:Title: Characterization of the rat mas oncogene and its high-level expression in the H
 A:Reference number: A31816; MUID:88276953; PMID:2455902
 A:Accession: A31816
 A:Molecule type: mRNA
 A:Residues: 1-324 <YOU>
 A:Cross-references: UNIPROT:P12526; UNIPARC:UP10000043DE7; GB:J03823; NID:G205313; PIDN:
 C:Genetics:
 A:Gene: mas
 C:Superfamily: mas transforming protein
 C:Keywords: G protein-coupled receptor; transforming protein; transmembrane protein
 F:31-47/Domain: transmembrane #status predicted <TM1>
 F:72-88/Domain: transmembrane #status predicted <TM2>
 F:149-165/Domain: transmembrane #status predicted <TM3>
 F:185-204/Domain: transmembrane #status predicted <TM4>
 F:225-243/Domain: transmembrane #status predicted <TM5>

Query Match 27.8%; Score 461; DB 1; Length 324;
 Best Local Similarity 33.9%; Pred. No. 1.7e-32;
 Matches 114; Conservative 64; Mismatches 118; Indels 40; Gaps 10;

1 MNOQTNSGTVESALNYSRG-----TYHTAYLVLSLAFMFCGAGNSMVTWLGFRM 56
 1 MDOSNMTSLAEKAMNTSSRNASLGSHPIPIVHWVMSISPVGEVNGILLMFLCFRRM 60
 57 HRNPFCTIYLNLAAADL-----LFLFSMASTLSLE-----TQPLVNTDKVHELMKRL 104
 61 RRPFTVYITHSLADISLFCIFILSDYALDYELSSGHYITVLSVT----- 110
 105 MYFATVGLSLTALSTORCLSVLPFWKCHRPRLHSAMVCGILMTCLLMGLTSSFC 164
 111 FLFGYNTGLYLTALTSVERCLSVLPYWRCHRPYHQSALFICALMLALCLVTTMEYVMC 170
 165 --SKLKNEDRCFRVDVQAALINGVLTPVWTLSSLTLPVWRRSSQWRQPTRLFVYV 222
 171 IDGSEHSQSDCRVYVIFIALISFLVFTPLMVLVSTLLVVKIRKNT--WASHSKLYIV 228
 223 VLASVLPFLCPLSLPIYFWVL--YMLSLPEMQVLCFSLSSSVSSANPVIYVGLG 280
 229 IMVTIITLPIFAMPKRVLYLYEYEWSTFGN-----LNHISLFTINSSANPFIYFVG 283
 281 SRRSHRLPRLSLGTYVQAALREE--PELEGGETPTV 314
 284 SSKKKRF-RESLKVVLTAFKDEQPRQEGNGNTV 318

RESULT 3
 TVHUS
 transforming protein mas - human
 C:Species: Homo sapiens (man)
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #next_change 09-Jul-2004
 C:Accession: A01375
 R:Young, D.; Waliches, G.; Birchmeier, C.; Faano, O.; Wigler, M.
 Cell 45, 711-719, 1986
 A:Title: Isolation and characterization of a new cellular oncogene encoding a protein w
 A:Reference number: A01375; MUID:86218084; PMID:3708691
 A:Accession: A01375
 A:Molecule type: DNA
 A:Residues: 1-325 <YOU>
 A:Cross-references: UNIPROT:P04201; UNIPARC:UP10000050458; GB:M13150; NID:G187388; PIDN:
 C:Genetics:
 A:Gene: GDB:MAS1
 A:Cross-references: GDB:120166; OMIM:165180
 A:Map position: 6q24-6q27
 C:Superfamily: mas transforming protein
 C:Keywords: G protein-coupled receptor; glycoprotein; proto-oncogene; transforming prote
 F:31-61/Domain: transmembrane #status predicted <TM1>
 F:66-97/Domain: transmembrane #status predicted <TM2>
 F:105-135/Domain: transmembrane #status predicted <TM3>
 F:150-172/Domain: transmembrane #status predicted <TM4>
 F:186-214/Domain: transmembrane #status predicted <TM5>

F:225-250/Domain: transmembrane #status predicted <TM6>
 F:258-286/Domain: transmembrane #status predicted <TM7>
 F:5,16,22,27/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.4%; Score 438.5; DB 1; Length 325;
 Best Local Similarity 33.6%; Pred. No. 1.5e-30;
 Matches 107; Conservative 58; Mismatches 114; Indels 39; Gaps 9;

7 SSGTVESALNYSRG-----STVHTAYLVLSLAFMFCGAGNSMVTWLGFRHRRPF 61
 7 TSFVVEEPTNISTGNASVGNARQIPVHWVMSISPVGEVNGILLMFLCFRRRRPF 66
 62 CIYIINLAAADL-----LFLFSMASTLSLE-----TQPLVNTDKVHELMKRLMVFAY 109
 67 TYVITHSLADISLFCIFILSDYALDYELSSGHYITVLSVT-----FLGKY 116
 110 TVGLSLTALSTORCLSVLPFWKCHRPRLHSAMVCGILMTCLLMGLTSSFCSEKTK 169
 117 NGLVLTALTSVERCLSVLPYWRCHRPYHQSALFICALMLALCLVTTMEYVMCIDREE 176
 170 FNEDR--CFRVDVQAALINGVLTPVWTLSSLTLPVWRRSSQWRQPTRLFVVLASV 227
 177 ESHSRNDCAVYIIFIALISFLVFTPLMVLVSTLLVVKIRKNT--WASHSKLYIYVNTI 234
 228 LVFLICSLPLSTYFWVL--YMLSLPEMQVLCFSLSSSVSSANPVIYVGLGRRSH 285
 235 IIFLIFAMPKRVLYLYEYEWSTFGN-----LNHISLFTINSSANPFIYFVGSKKK 289
 286 RLPTSLGTYVQAALREE 303
 290 RF-KESLKVVLTAFKDE 306

RESULT 4
 S51001
 transforming protein mas - mouse
 N:Alternate names: mas proto-oncogene protein; probable G protein-coupled receptor mas
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #next_change 09-Jul-2004
 C:Accession: S51001; 148647; S29619
 R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.
 FEBS Lett. 357, 27-32, 1995
 A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral
 A:Reference number: 148647; MUID:95094925; PMID:8001672
 A:Accession: S51001; MUID:95094925; PMID:8001672
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-324 <MET>
 A:Cross-references: UNIPROT:P30554; UNIPARC:UP1000003B44B; EMBL:X67735
 R:Metzger, R.; Bader, M.; Ludwig, T.; Berberich, C.; Bunnemann, B.; Ganten, D.
 FEBS Lett. 357, 27-32, 1995
 A:Title: Expression of the mouse and rat mas proto-oncogene in the brain and peripheral
 A:Reference number: 148647; MUID:95094925; PMID:8001672
 A:Accession: S51001; MUID:95094925; PMID:8001672
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-87, '1', 89-324 <RES>
 A:Cross-references: UNIPARC:UP10000029856; EMBL:X67735; NID:G53011; PIDN:CAA47964.1; PI
 C:Genetics:
 A:Gene: mas
 C:Superfamily: mas transforming protein
 C:Keywords: G protein-coupled receptor; proto-oncogene; transmembrane protein

Query Match 26.3%; Score 437; DB 2; Length 324;
 Best Local Similarity 33.8%; Pred. No. 1.e-30;
 Matches 116; Conservative 61; Mismatches 112; Indels 54; Gaps 12;

1 MNOQTNSGTVESALNYSR-----GST-----YHTAYLVLSLAFMFCGAGNSMVI 49
 1 MDOSNMTSLAEKAMNTSSRNASLGSHPIPIVHWVMSISPV-----GFVNGILL 53
 50 WLQGRHRNPFCTIYLNLAAADLFLFSMASTLSLETQPLVNTDKV--HELMKRLMY- 106

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 09:57:49 ; Search time 28 Seconds
(without alignments)

538.235 Million cell updates/sec

Title: US-10-509-484-4

Perfect score: 1661
1 MNQTLNNGSGVYESALNYSRSG.....EEPELBEGETPTVGTNEMGA 321

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /SIDS5/ptodata/1/pubppaa/US08_NEW_PUB.pep1.*
- 2: /SIDS5/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 3: /SIDS5/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /SIDS5/ptodata/1/pubppaa/US05_NEW_PUB.pep.*
- 5: /SIDS5/ptodata/1/pubppaa/US04_NEW_PUB.pep.*
- 6: /SIDS5/ptodata/1/pubppaa/US03_NEW_PUB.pep.*
- 7: /SIDS5/ptodata/1/pubppaa/US02_NEW_PUB.pep1.*
- 8: /SIDS5/ptodata/1/pubppaa/US10_NEW_PUB.pep1.*
- 9: /SIDS5/ptodata/1/pubppaa/US10_NEW_PUB.pep1.*
- 10: /SIDS5/ptodata/1/pubppaa/US11_NEW_PUB.pep1.*
- 11: /SIDS5/ptodata/1/pubppaa/US11_NEW_PUB.pep1.*
- 12: /SIDS5/ptodata/1/pubppaa/US60_NEW_PUB.pep1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1661	100.0	321	9	US-10-509-484-4
2	912.5	54.9	319	9	US-10-509-484-2
3	544.5	32.8	322	9	US-10-747-702-13
4	539.5	32.5	322	9	US-10-747-702-11
5	537.5	32.4	322	9	US-10-747-702-9
6	537	32.3	322	9	US-10-747-702-7
7	525	31.6	337	9	US-10-747-702-1
8	522	31.4	330	9	US-10-332-186-1
9	510	30.7	322	9	US-10-747-702-3
10	501	30.2	330	11	US-11-206-587-8
11	492	29.6	322	9	US-10-747-702-5
12	481.5	29.0	343	9	US-10-055-877-244
13	481.5	29.0	343	9	US-10-055-877-245
14	476.5	28.7	343	9	US-10-055-877-71
15	465.5	28.0	342	9	US-10-055-877-246
16	462.5	27.8	311	9	US-10-980-388-111
17	462.5	27.8	310	9	US-10-980-388-62
18	462	27.8	311	9	US-10-980-388-113
19	451.5	27.2	319	9	US-10-055-877-247
20	416	25.0	340	9	US-10-055-877-69
21	364	21.9	323	9	US-10-980-388-119

22	270.5	16.3	187	9	US-10-980-388-39	Sequence 39, Appl
23	270.5	16.3	187	9	US-10-980-388-98	Sequence 98, Appl
24	269.5	16.2	349	9	US-10-237-813-24	Sequence 24, Appl
25	257.5	15.5	353	9	US-10-508-765-2	Sequence 2, Appl1
26	257.5	15.5	353	9	US-10-237-813-13	Sequence 13, Appl
27	255.5	15.4	349	9	US-10-237-813-14	Sequence 14, Appl
28	254.5	15.3	349	9	US-10-237-813-15	Sequence 15, Appl
29	253.5	15.3	353	11	US-11-218-281-25	Sequence 25, Appl
30	253.5	15.3	353	11	US-11-129-107-2	Sequence 2, Appl1
31	245.5	14.8	349	9	US-10-237-813-16	Sequence 16, Appl
32	243	14.6	356	9	US-10-237-813-21	Sequence 21, Appl
33	243	14.6	356	11	US-11-218-281-27	Sequence 27, Appl
34	241.5	14.5	211	9	US-10-980-388-97	Sequence 97, Appl
35	240.5	14.5	350	9	US-10-502-145-1	Sequence 1, Appl1
36	240.5	14.5	350	9	US-10-237-813-22	Sequence 22, Appl
37	240.5	14.5	350	11	US-11-169-976-9	Sequence 9, Appl1
38	240.5	14.5	350	11	US-11-218-281-31	Sequence 31, Appl
39	239	14.4	395	9	US-10-237-813-23	Sequence 23, Appl
40	239	14.4	395	11	US-11-218-281-29	Sequence 29, Appl
41	239	14.4	395	11	US-11-296-524-2	Sequence 2, Appl1
42	239	14.4	395	11	US-11-296-524-8	Sequence 8, Appl1
43	230	13.8	371	9	US-10-237-813-5	Sequence 5, Appl1
44	230	13.8	371	11	US-11-134-811-4	Sequence 4, Appl1
45	230	13.8	371	11	US-11-218-281-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1

US-10-509-484-4

Sequence 4, Application US/10509484

Publication No. US20060073516A1

GENERAL INFORMATION:

APPLICANT: Takeda Chemical Industries, Ltd.

TITLE OF INVENTION: Novel Screening Method

FILE REFERENCE: R04-117PCT

CURRENT APPLICATION NUMBER: US/10/509,484

CURRENT FILING DATE: 2004-09-27

PRIOR APPLICATION NUMBER: JP 2002-093045

PRIOR FILING DATE: 2002-03-28

PRIOR APPLICATION NUMBER: JP 2002-361580

PRIOR FILING DATE: 2002-12-13

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 321

TYPE: PRT

ORGANISM: Homo sapiens

US-10-509-484-4

Query Match 100.0%; Score 1661; DB 9; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-139;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNQTLLNGSGVYESALNYSRSGTHTATLVUSLSLAMPFTCLCGMAGNSWVTLGFRMRNP	60
DB	1	MNQTLLNGSGVYESALNYSRSGTHTATLVUSLSLAMPFTCLCGMAGNSWVTLGFRMRNP	60
QY	61	FCITLLMLAADDLFLFSMASTLSLETQPLVNTTQKHEHMKMLPAVTVGLSLTAIS	120
DB	61	FCITLLMLAADDLFLFSMASTLSLETQPLVNTTQKHEHMKMLPAVTVGLSLTAIS	120
QY	121	TORCLSLVLPFWFKRPHLSAVCGLLMTLCLMNGLTSSFCSEKLEKNEDECFEVD	180
DB	121	TORCLSLVLPFWFKRPHLSAVCGLLMTLCLMNGLTSSFCSEKLEKNEDECFEVD	180
QY	181	VOALLINGVLTPTVNTLSLTFVWVRSSSQOMRQPRFLRVVVLASLVVLICSLPISTY	240
DB	181	VOALLINGVLTPTVNTLSLTFVWVRSSSQOMRQPRFLRVVVLASLVVLICSLPISTY	240
QY	241	MFVLYMLSLPEKMOVLQFSLSSSVSSSNPIYFLVGSRRSHRPLTSLGLVQAL	300
DB	241	MFVLYMLSLPEKMOVLQFSLSSSVSSSNPIYFLVGSRRSHRPLTSLGLVQAL	300

Db 241 WFLVWMLSPPEMOVLCPFSLSRLSSVSSANPVIYFLVGSRRSHRLPTRSLGTVLQAL 300
Qy 301 REEPELEGGETPTVTGTMEMGA 321
Db 301 REEPELEGGETPTVTGTMEMGA 321

RESULT 4

US-10-509-484-2
; Sequence 2, Application US/10509484
; Publication No. US20060073516A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Novel Screening Method
; FILE REFERENCE: P04-117PCT
; CURRENT APPLICATION NUMBER: US/10/509,484
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: JP 2002-093045
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: JP 2002-361580
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-509-484-2

Query Match 54.9%; Score 912.5; DB 9; Length 319;
Best Local Similarity 58.5%; Pred. No. 2.4e-73;
Matches 190; Conservative 48; Mismatches 72; Indels 15; Gaps 6;

Qy 1 MNQTLNNGSG---TVESALNYSRSGSTVHTAYLVLSLAMPFCICGAGNSMVTMLGFR- 55
Db 1 MNVTPYSSPADGLTISPTMD-----PVTWYFVSYFLFAMATCGVIGNSMVTMLSFHS 55
Qy 56 MHRNPFICYIINLAAADLLFLFSMASTLSLETOPLV--NTTDKVMELMKRLMYFAYTVGL 113
Db 56 VQSPFCTYVNLNADLLFLCMAASLSLETPILTSTARSAYEGSKRIKRYAYTAGL 115
Qy 114 SLTAISTORCLSVLPFWFKCHPRRLSAAVCGLLMTLCLMNGLTSSFCSEKFLKRNED 173
Db 116 SLTAISTORCLSVLPFWFKCHPRRLSAAVCGLLMTLCLMNGLTSSFCSEKFLKRNED 175
Qy 174 RCFRVDYQALIMGVLPVMTLSLTFVWVRSSQQRROP-TRLFVVLASVLPFLCGL 233
Db 176 QCFKVDYQALIMGVLPVMTLSLTFVWVRSSQQRROP-TRLFVVLASVLPFLCGL 235
Qy 234 SLPISTIYFVLVWMLSPPEMOVLCPFSLSRLSSVSSANPVIYFLVGSRRSHRLPTRSLG 293
Db 236 SLPISTIYFVLVWMLSPPEMOVLCPFSLSRLSSVSSANPVIYFLVGSRRSHRLPTRSLG 294
Qy 294 TVLQALREPELEGGETPTVTGTM 318
Db 295 AVLGRLQDEP--EREETPSTCTND 317

RESULT 3

US-10-747-702-13
; Sequence 13, Application US/10747702
; Publication No. US20060068466A1
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G-Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/10/747,702
; CURRENT FILING DATE: 2003-12-30

; PRIOR APPLICATION NUMBER: Prio APPLICATION NUMBER: US/09/254,227
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-747-702-13

Query Match 32.8%; Score 544.5; DB 9; Length 322;
Best Local Similarity 41.9%; Pred. No. 8.9e-41;
Matches 134; Conservative 56; Mismatches 105; Indels 25; Gaps 10;

Qy 1 MNQTLNNGSGTVESALNYSRSGSTVHTAYLVLSLAMPFCICGAGNSMVTMLGFRMRNP 60
Db 1 MDPVTVFVGTGLTPINGRETEPCYNOTLSFTVLTCTISLVELTGNNAVVMGLGRMRRA 60
Qy 61 FCYIINLAAADLLFLFSMASTLSLETOP--LVNTTDKVMELMKRLMYFAYTVGSLTA 118
Db 61 VSIYIINLAAADLLFLFSMASTLSLETOP--LVNTTDKVMELMKRLMYFAYTVGSLTA 115
Qy 119 ISTORCLSVLPFWFKCHPRRLSAAVCGLLMTLCLMNGLTSSFCSEKFLKRNED--CF 176
Db 116 ISTORCLSVLPFWFKCHPRRLSAAVCGLLMTLCLMNGLTSSFCSEKFLKRNED--CF 174
Qy 177 RVDVQALIMGVLPVMTLSLTFVWVRSSQQRROP-TRLFVVLASVLPFLCGL 235
Db 175 TSDPIPVWLI--FLCVLVCSSLVLPVRLCGS--RKMPRLRYVITLITLVLPFLCGL 230
Qy 236 PLSTIYFVLVWMLSPPE---MQVLCFSLSLSSVSSANPVIYFLVGSRRSHRLPTR 290
Db 231 PEGILGALYRMHNLNEVLYCHVLYCWSL---SLNSANPDIYFVGSFR--QRONRO 285
Qy 291 SLGTVLOALREPELEGGE 310
Db 286 NKLTVLORALQDEPKGE 305

RESULT 4

US-10-747-702-11
; Sequence 11, Application US/10747702
; Publication No. US20060068466A1
; GENERAL INFORMATION:
; APPLICANT: Ahmad, Sultan
; APPLICANT: Banville, Denis
; APPLICANT: Fortin, Yves
; APPLICANT: Lembo, Paola
; APPLICANT: O'Donnell, Dajan
; APPLICANT: Shi-Hsiang, Shen
; TITLE OF INVENTION: G-Protein-Coupled Receptors from the Rat and Human
; FILE REFERENCE: 81823/268117
; CURRENT APPLICATION NUMBER: US/10/747,702
; CURRENT FILING DATE: 2003-12-30
; PRIOR APPLICATION NUMBER: Prio APPLICATION NUMBER: US/09/254,227
; PRIOR FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-747-702-11

Query Match 32.5%; Score 539.5; DB 9; Length 322;
Best Local Similarity 42.4%; Pred. No. 2.5e-40;
Matches 137; Conservative 54; Mismatches 101; Indels 31; Gaps 12;

Qy 1 MNQTLNNGSGTVESALNYSRSGSTVHTAYLVLSLAMPFC---LTCGAGNSMVTMLGFRMRNP 57
Db 1 MDPVTVFVGTGLTPIN---GRETEPCYKOTLSFTVLTCTISLVELTGNNAVVMGLGRMR 57
Qy 58 RNPFCYIINLAAADLLFLFSMASTLSLETOP--LVNTTDKVMELMKRLMYFAYTVGSL 115

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 11, 2006, 09:49:03 ; Search time 230 Seconds

(without alignments)
984.672 Million cell updates/sec

Title: US-10-509-484-4

Perfect score: 1661
Sequence: 1 MNQTLNNSGTVESALNYSRG.....EPELEGGERTVTGTEMGA 321

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 216643 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 216643

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt 05.80:*

1: uniprot_sprot:*
2: uniprot_trnsl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1661	100.0	321	1	MRGD_HUMAN
2	1440.5	86.7	327	2	OSU9D6_MACFA
3	1439.5	86.7	320	1	MRGD_MACFA
4	921.5	55.5	321	1	MRGD_MOUSE
5	921.5	55.5	321	2	OSUCB4_MOUSE
6	917.5	55.2	319	1	MRGRD_RAT
7	548.5	33.0	322	1	MRGX4_HUMAN
8	544.5	32.8	322	1	SNSR5_HUMAN
9	542	32.6	322	1	SNSR3_HUMAN
10	538.5	32.4	322	1	MRGX1_HUMAN
11	538.5	32.4	322	2	Q4V9L2_HUMAN
12	538	32.4	329	2	Q4QXU5_MACMU
13	537.5	32.4	322	2	OSU9D6_MACFA
14	532	32.0	330	2	Q4QXU2_PYGRI
15	528.5	31.8	332	2	Q4QXU5_MACFA
16	528.5	31.8	330	1	MRGX2_MACFA
17	525	31.6	323	2	Q7TN42_RAT
18	524.5	31.6	330	2	Q4QXU4_TRAFR
19	524.5	31.6	329	2	Q4QXU5_PANTR
20	522.5	31.5	329	2	Q4QXU0_GPRIM
21	522	31.4	330	1	MRGX2_HUMAN
22	521	31.4	330	2	SNSR1_RAT
23	519	31.2	330	2	Q4QXU7_HUMAN
24	518.5	31.2	332	2	OSU9D6_MOUSE
25	517	31.1	330	2	Q4QXU6_HUMAN
26	517	31.1	330	2	Q4QXU2_HUMAN
27	515.5	31.0	330	2	Q7TN45_RAT
28	515	31.0	330	2	Q4QXU4_HUMAN
29	515	31.0	330	2	Q4QXU7_HUMAN
30	514.5	31.0	330	2	Q4QXU3_HUMAN
31	514.5	31.0	330	2	Q4QXU3_HUMAN

32	514	30.9	321	2	Q91ZC0_MOUSE
33	512.5	30.9	330	2	Q4QXU0_HUMAN
34	511.5	30.8	330	2	Q4QXU3_PONPY
35	509.5	30.7	329	2	Q4QXU6_GPRIM
36	508	30.6	332	1	MRGX3_MOUSE
37	506	30.5	332	1	MRGX3_HUMAN
38	503	30.3	330	1	MRGX1_MOUSE
39	500.5	30.1	331	2	OSU9D6_MOUSE
40	499	30.0	330	1	MRGX4_RAT
41	499	30.0	331	2	Q91YB7_RAT
42	494.5	29.8	313	1	MRGX4_MOUSE
43	493.5	29.7	305	1	MRGX8_MOUSE
44	492	29.6	294	2	Q7TN48_RAT
45	492	29.6	322	1	SNSR2_HUMAN

ALIGNMENTS

RESULT 1
MRGD_HUMAN STANDARD; PRT; 321 AA.
ID MRGD_HUMAN
AC Q8TDS7; Q8NGK7;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Mas-related G-protein coupled receptor member D (Beta-alanine receptor) (G-protein coupled receptor TGR7).
GN Name=MRGPRD; Synonyms=MRGD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
OX NCB1; TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE. PubMed=12909716; DOI=10.1073/pnas.1732949100;
RX MEDLINE=22810130; PubMed=12909716; DOI=10.1073/pnas.1732949100;
RA Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
RT "Atypical expansion in mice of the sensory neuron-specific Mrg G protein-coupled receptor family";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE, SUBCELLULAR LOCATION, AND POSSIBLE FUNCTION.
RC TISSUE=Liver;
RX PubMed=15037633; DOI=10.1074/jbc.M314240200;
RA Shinozaki T., Harada M., Ogi K., Maruyama M., Fujii R., Tanaka H., Fukusumi S., Komatsu H., Hosoya M., Noguchi Y., Watanabe T., Moriya T., Itoh Y., Hinuma S.;
RT "Identification of a G protein-coupled receptor specifically responsive to beta-alanine";
RL J. Biol. Chem. 279:23559-23564(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human genome sequence";
RL FEBS Lett. 520:97-101(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Suwa M., Sato T., Okouchi I., Arita M., Putani K., Matsumoto S., Tetsutani S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix receptor genes";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May regulate nociceptor function and/or development, including the sensation or modulation of pain. Functions as a specific membrane receptor for beta-alanine. Beta-alanine at micromolar doses specifically evoked Ca(2+) influx in cells expressing the receptor. Beta-alanine decreases forskolin-stimulated cAMP production in cells expressing the receptor, suggesting that the receptor couples with G-protein G(q) and G(i).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Localized at the

CC plasma membrane but internalized into the cytoplasm after
 CC treatment with beta-alanine
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC Was subfamily.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC usage as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AY427820; AAR05120.1; -; mRNA.
 CC EMBL: AB154410; BAD20638.1; -; mRNA.
 CC EMBL: AB083627; BAB89340.1; -; Genomic DNA.
 CC EMBL: AB065786; BAC06005.1; ALT_INIT; Genomic DNA.
 CC EMBL: ENSG00000172938; Homo sapiens.
 CC HGN: HGNC:29626; MRGPRD.
 CC MIM: 607231; -.
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCR_Rhodopsn.
 CC PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
 CC PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 CC Transmembrane.
 CC -----
 CC TOPO_DOM 1 33 Extracellular (Potential).
 CC TRANSMEM 34 54 1 (Potential).
 CC TRANSMEM 55 59 Cytoplasmic (Potential).
 CC TOPO_DOM 60 80 2 (Potential).
 CC TRANSMEM 81 112 Extracellular (Potential).
 CC TOPO_DOM 113 133 3 (Potential).
 CC TRANSMEM 134 142 Cytoplasmic (Potential).
 CC TOPO_DOM 143 163 4 (Potential).
 CC TRANSMEM 164 184 Extracellular (Potential).
 CC TOPO_DOM 185 205 5 (Potential).
 CC TRANSMEM 206 218 Cytoplasmic (Potential).
 CC TOPO_DOM 219 239 6 (Potential).
 CC TRANSMEM 240 257 Extracellular (Potential).
 CC TOPO_DOM 258 280 7 (Potential).
 CC TRANSMEM 281 321 Cytoplasmic (Potential).
 CC CARBOHYD 2 2 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 6 6 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 16 16 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 92 92 N-linked (GlcNAc...) (Potential).
 CC SEQUENCE 321 AA; 36118 MW; B45AB7FEB2154B40 CRC64;
 CC -----
 CC Query Match 100.0%; Score 1661; DB 1; Length 321;
 CC Best Local Similarity 100.0%; Pred. No. 7.6e-120;
 CC Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 ID Q509D8_MACFA PRELIMINARY; PRT; 337 AA.
 AC Q509D8;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Mac-related protein D.
 GN Name=MrgD;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Zhang L., Taylor N., Ford R., Johnson J., Paulsen J.E., Bates B.,
 RT "Cloning and Expression of MRG Receptors in Macaque, Mouse, and
 RT Human."
 RU Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC EMBL: AY772459; AA49126.1; -; Genomic DNA.
 CC GO: GO:0016021; C:integral to membrane; IEA.
 CC GO: GO:0004872; F:receptor activity; IEA.
 CC GO: GO:0001584; F:rhodopsin-like receptor protein signaling; IEA.
 CC GO: GO:0007186; P:G-protein coupled receptor protein signaling; IEA.
 CC GO: GO:0007165; P:signal transduction; IEA.
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCR_Rhodopsn.
 CC PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 CC SEQUENCE 337 AA; 37776 MW; D41CDBA565EABE5 CRC64;
 CC -----
 CC Query Match 86.7%; Score 1440.5; DB 2; Length 337;
 CC Best Local Similarity 88.2%; Pred. No. 7.6e-103;
 CC Matches 283; Conservative 13; Mismatches 24; Indels 1; Gaps 1;